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FIG. 1A

GAATTCTCTGGACTGAGGCTCCAGTTCTGGCCTTTGGGG

TTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCCCCGAGTCTCAACCCTCAACTGTC

ACCCCAAGGCACTTGGGACGTCCTGGACAGACCGAGTCCCGGGAAGCCCCAGCACTGCC

GCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAGGCCA TAG CTG TCT GGC

S1				S5					S10				S15
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu													
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG CTC													
216				225				234			243		252

				S20					S25			S29	1
Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu													
CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG													
261				270				279			288		297

			5					10					15
Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro													
GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC													
306			315				324			333			342

			20					25					30
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr													
CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC													
351			360				369			378			387

			35					40					45
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro													
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG													
396			405				414			423			432

			50					55					60
Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr													
GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC													
441			450				459			468			477

			65					70					75
Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys													
GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC													
486			495				504			513			522

			80					85					90
Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp													
CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC													
531			540				549			558			567

FIG. 1A

FIG. 1B

			95						100						105		
Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His	Tyr			
CGG	GAC	ACC	GTG	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT			
576			585			594			603			612					
			110						115						120		
Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu	Cys	Leu			
TGG	AGT	GAA	AAC	CTT	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC			
621			630			639			648			657					
			125						130						135		
Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val			
AAT	GGG	ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG			
666			675			684			693			702					
			140						145						150		
Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val			
TGC	ACC	TGC	CAT	GCA	GGT	TTC	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC			
711			720			729			738			747					
			155						160						165		
Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	Lys	Leu	Cys			
TCC	TGT	AGT	AAC	TGT	AAG	AAA	AGC	CTG	GAG	TGC	ACG	AAG	TTG	TGC			
756			765			774			783			792					
			170						175						180		
Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	Gly	Thr			
CTA	CCC	CAG	ATT	GAG	AAT	GTT	AAG	GGC	ACT	GAG	GAC	TCA	GGC	ACC			
801			810			819			828			837					
			185						190						195		
Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	Leu			
ACA	GTG	CTG	TTG	CCC	CTG	GTC	ATT	TTC	TTT	GGT	CTT	TGC	CTT	TTA			
846			855			864			873			882					
			200						205						210		
Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys			
TCC	CTC	CTC	TTC	ATT	GGT	TTA	ATG	TAT	CGC	TAC	CAA	CGG	TGG	AAG			
891			900			909			918			927					
			215						220						225		
Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys			
TCC	AAG	CTC	TAC	TCC	ATT	GTT	TGT	GGG	AAA	TCG	ACA	CCT	GAA	AAA			
936			945			954			963			972					
			230						235						240		
Glu	Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn			
GAG	GGG	GAG	CTT	GAA	GGA	ACT	ACT	ACT	AAG	CCC	CTG	GCC	CCA	AAC			
981			990			999			1008			1017					

FIG. 1B

FIG. 1C

Pro	Ser	Phe	245	Ser	Pro	Thr	Pro	Gly	250	Phe	Thr	Pro	Thr	Leu	Gly	Phe	255
CCA	AGC	TTC	AGT	CCC	ACT	CCA	GGC	TTC	ACC	CCC	ACC	CTG	GGC	TTC			
1026			1035			1044			1053			1062					
Ser	Pro	Val	260	Pro	Ser	Ser	Thr	Phe	265	Thr	Ser	Ser	Ser	Thr	Tyr	Thr	270
AGT	CCC	GTG	CCC	AGT	TCC	ACC	TTC	ACC	TCC	AGC	TCC	ACC	TAT	ACC			
1071			1080			1089			1098			1107					
Pro	Gly	Asp	275	Cys	Pro	Asn	Phe	Ala	280	Pro	Arg	Arg	Glu	Val	Ala		
CCC	GGT	GAC	TGT	CCC	AAC	TTT	CGC	GCT	CCC	CGC	AGA	GAG	GTG	GCA			
1116			1125			1134			1143			1152					
Pro	Pro	Tyr	290	Gln	Gly	Ala	Asp	Pro	295	Ile	Leu	Ala	Thr	Ala	Leu	Ala	
CCA	CCC	TAT	CAG	GGG	GCT	GAC	CCC	ATC	CTT	GCG	ACA	GCC	CTC	GCC			
1161			1170			1179			1188			1197					
Ser	Asp	Pro	305	Ile	Pro	Asn	Pro	Leu	310	Gln	Lys	Trp	Glu	Asp	Ser	Ala	
TCC	GAC	CCC	ATC	CCC	AAC	CCC	CTT	CAG	AAG	TGG	GAG	GAC	AGC	GCC			
1206			1215			1224			1233			1242					
His	Lys	Pro	320	Gln	Ser	Leu	Asp	Thr	325	Asp	Asp	Pro	Ala	Thr	Leu	Tyr	
CAC	AAG	CCA	CAG	AGC	CTA	GAC	ACT	GAT	GAC	CCC	GCG	ACG	CTG	TAC			
1251			1260			1269			1278			1287					
Ala	Val	Val	335	Glu	Asn	Val	Pro	Pro	340	Leu	Arg	Trp					
GCC	GTG	GTG	GAG	AAC	GTG	CCC	CCG	TTG	CGC	TGG	AA	<u>GGAATTC</u>					
1296			1305			1314			1323			1332					

FIG. 1C

FIG. 2

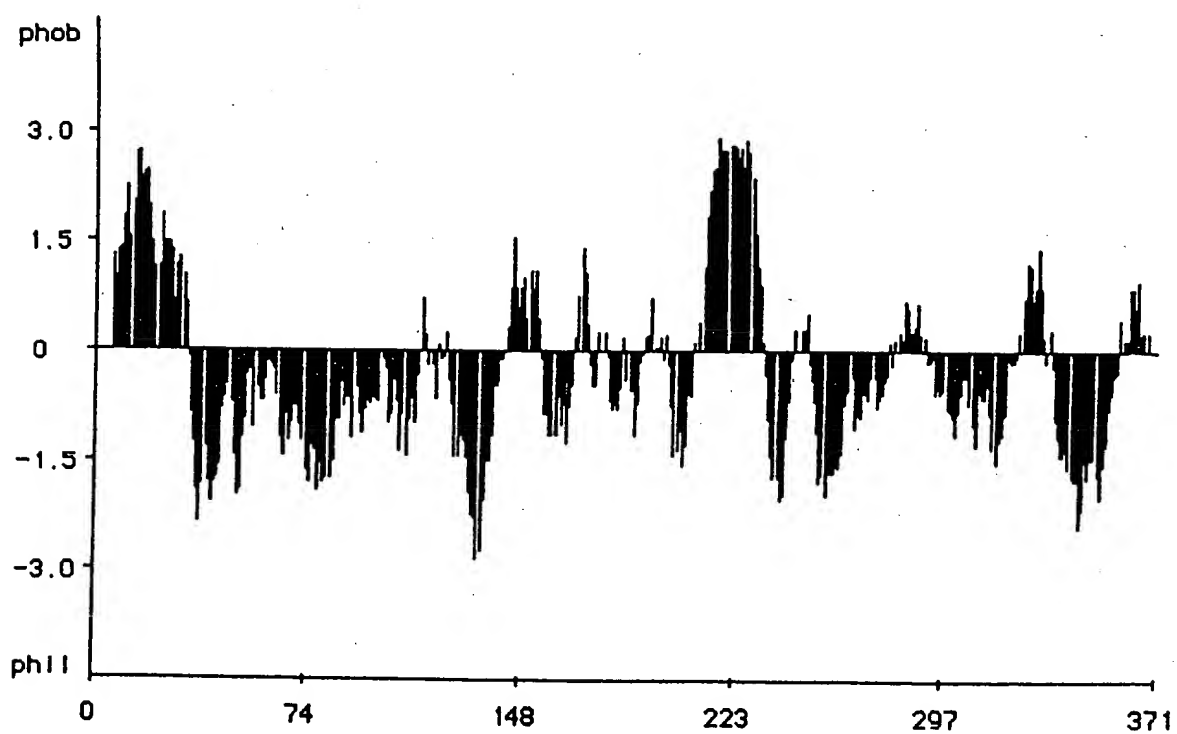


FIG. 3A

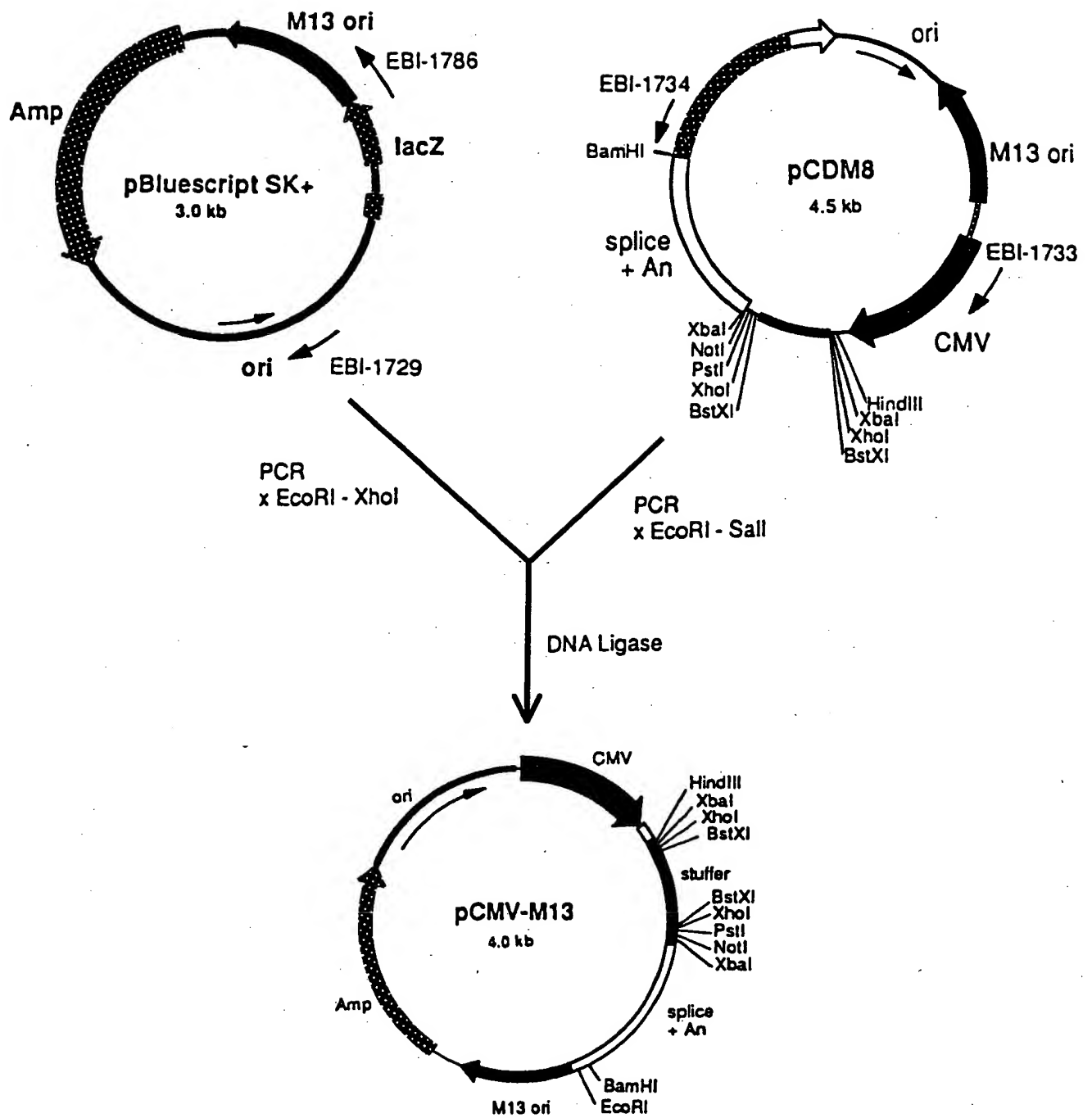


FIG. 3B

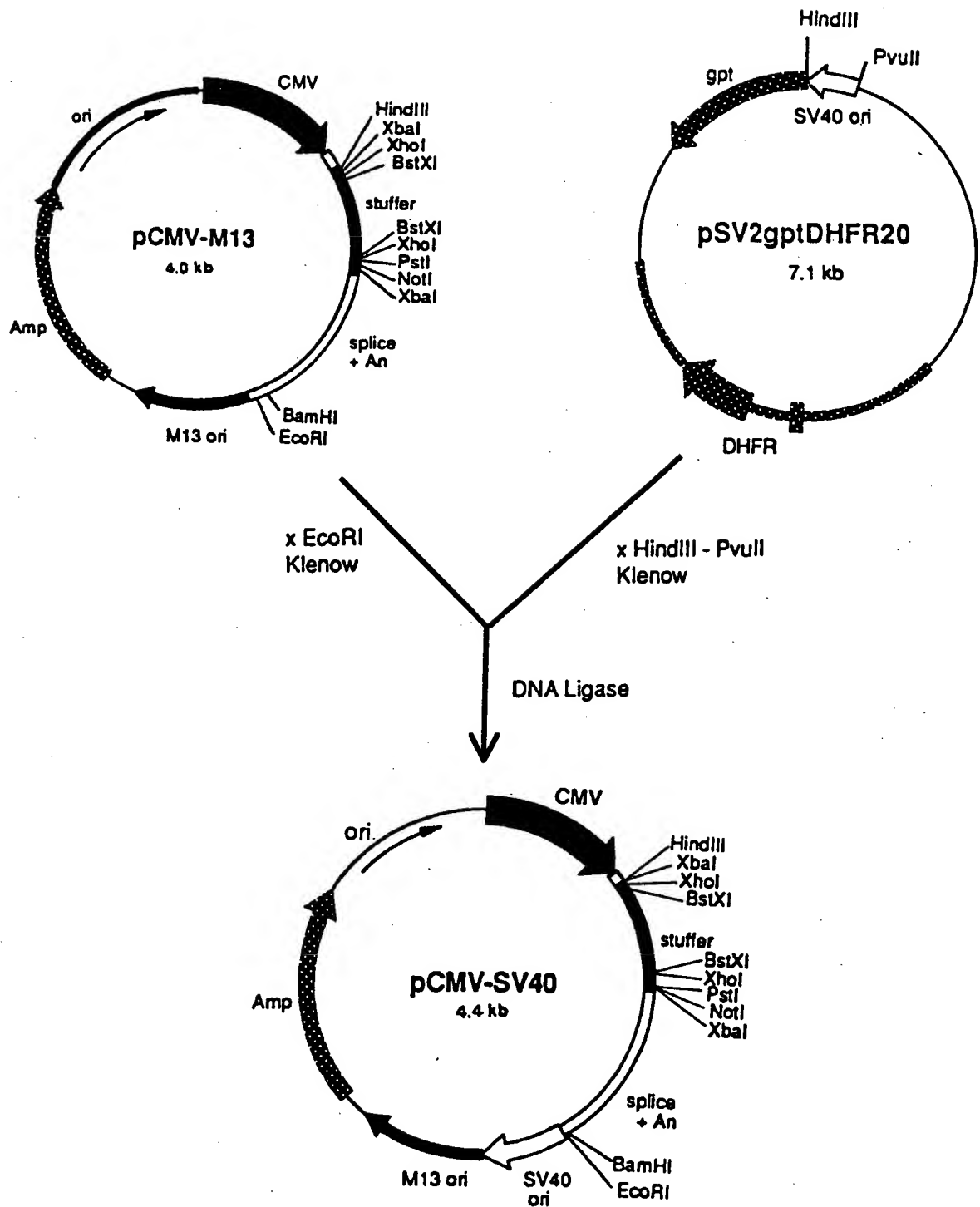


FIG. 4A

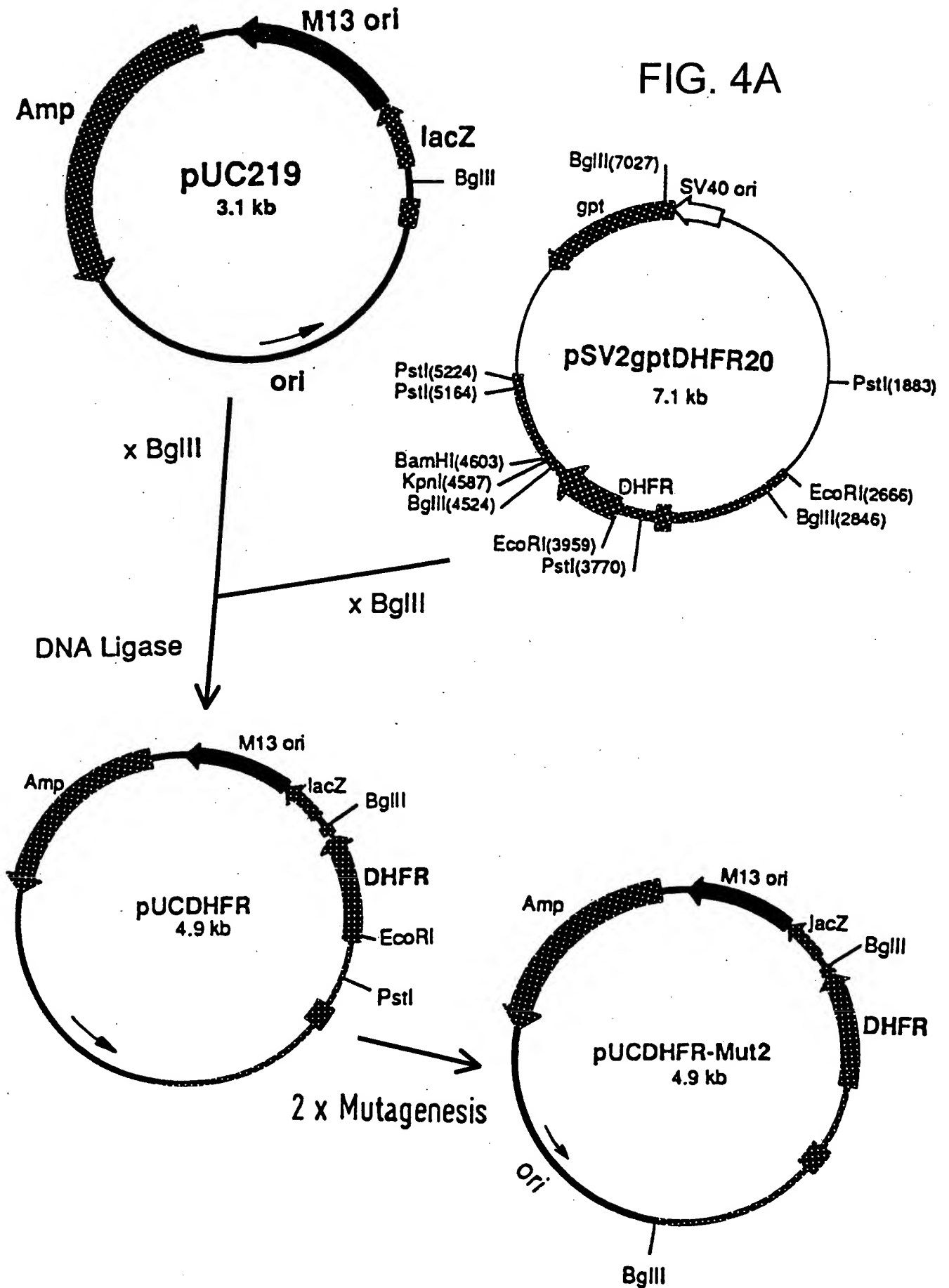
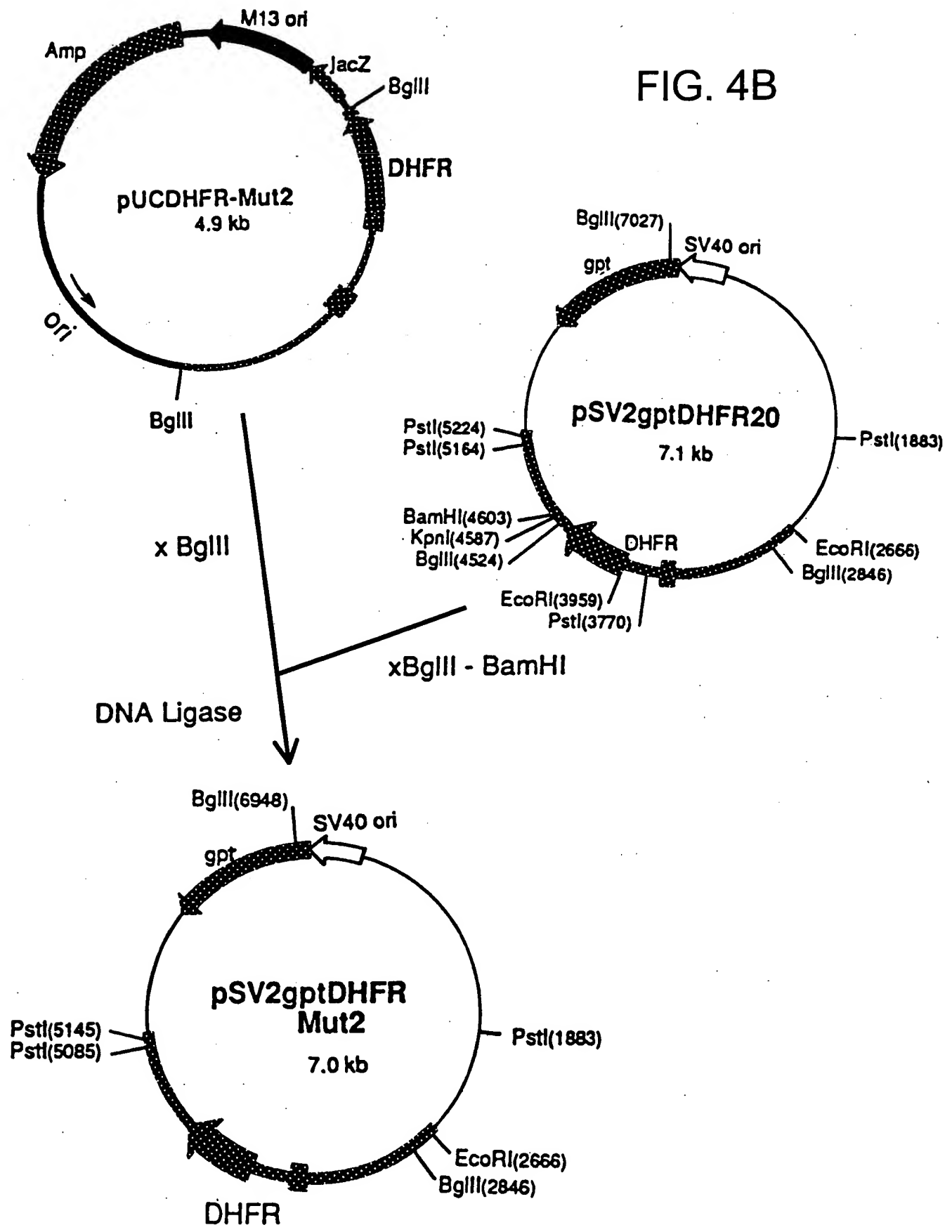


FIG. 4B

FIG. 4B



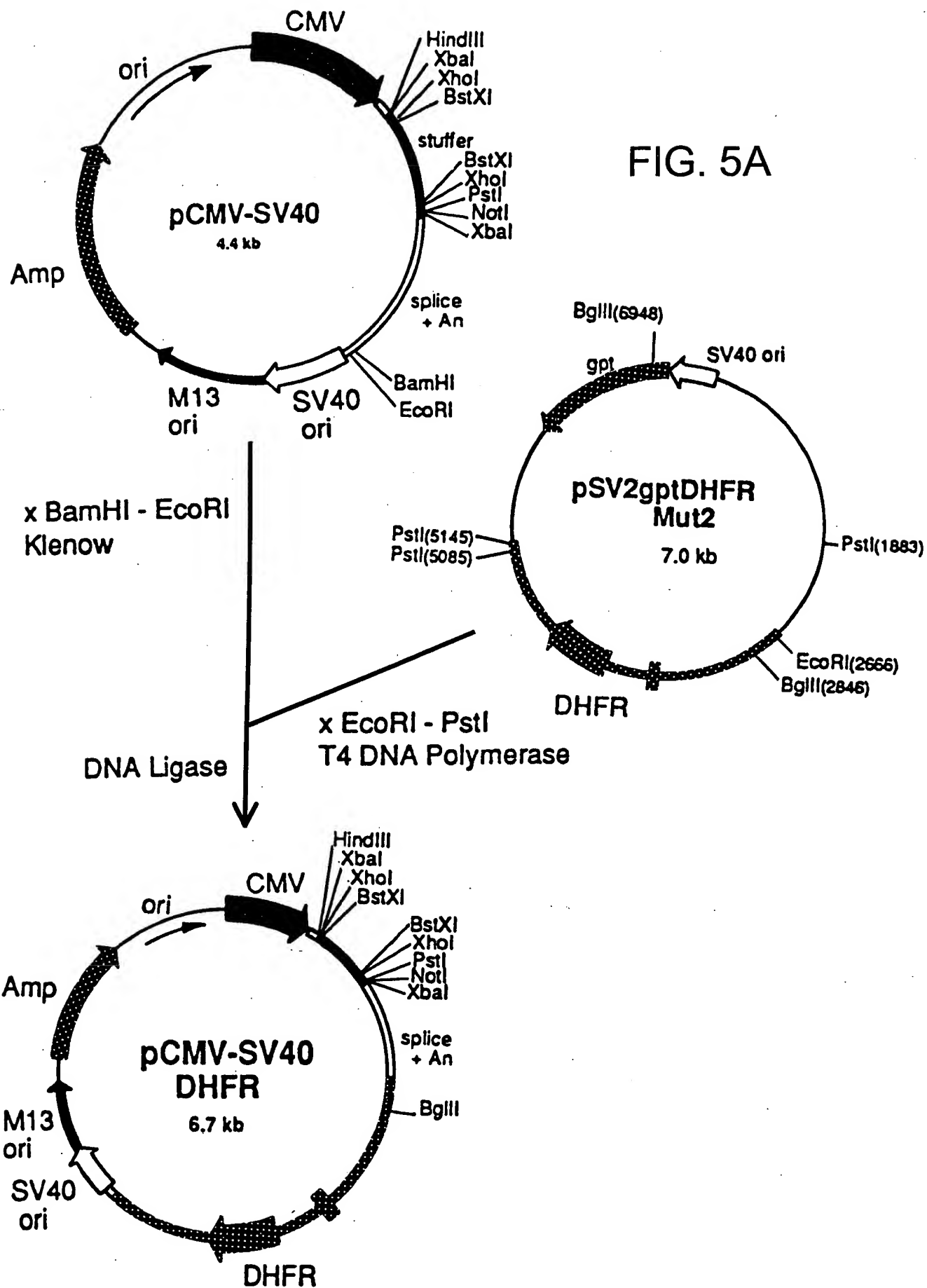


FIG. 5B

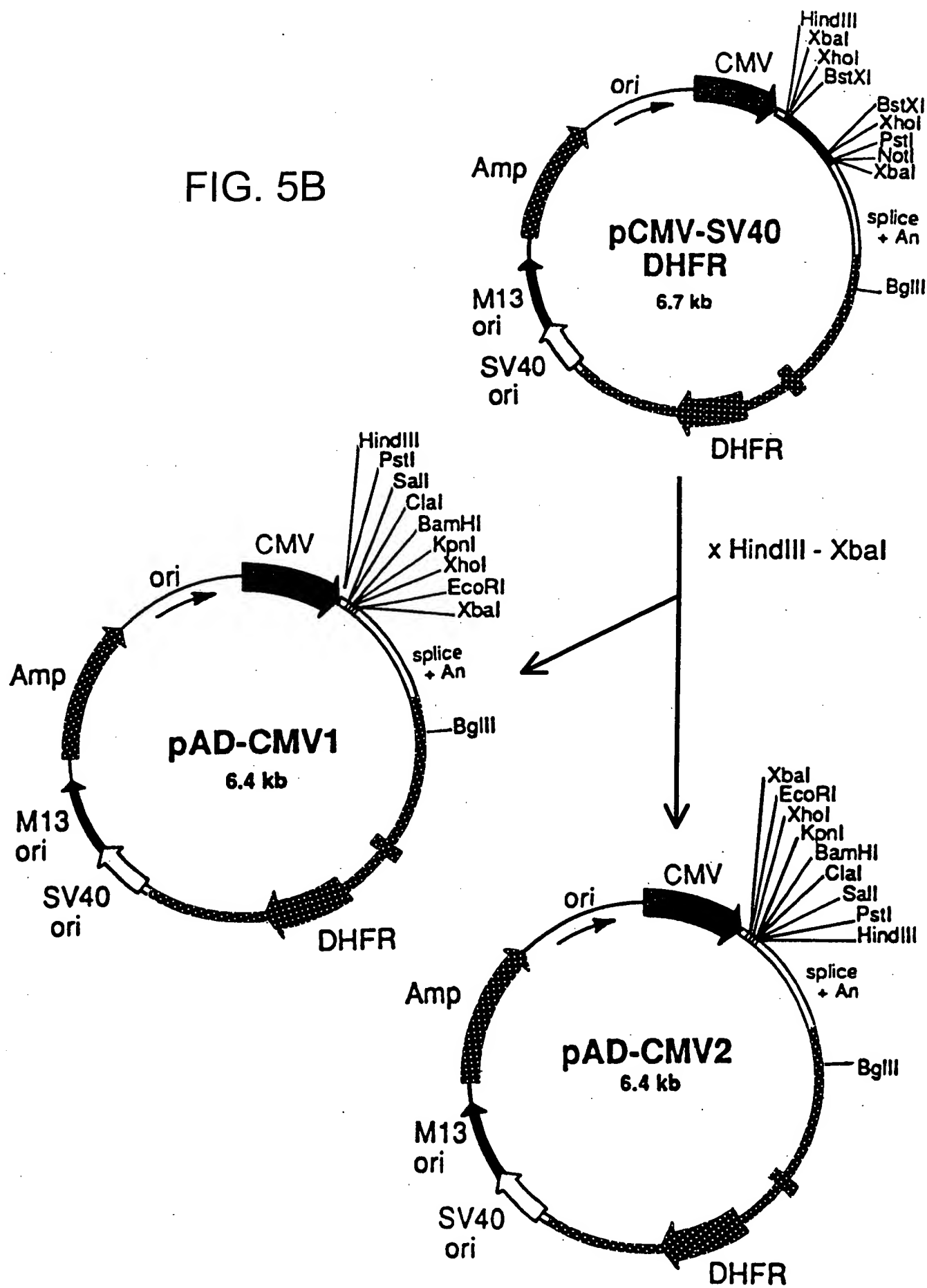


FIG. 6A

pAD-CMV1 : 6414 bp

TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT TAGTTCATAG	60
CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT GGCCCGCCTG GCTGACCGCC	120
CAACGACCCC CGCCCATTGA CGTCAATAAT GACGTATGTT CCCATAGTAA CGCCAATAGG	180
GACTTTCCAT TGACGTCAAT GGGTGGAGTA TTTACGGTAA ACTGCCCACT TGGCAGTACA	240
TCAAGTGTAT CATATGCCAA GTACGCCCCC TATTGACGTC AATGACGGTA AATGGCCCCG	300
CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTTGGCAGT ACATCTACGT	360
ATTAGTCATC GCTATTACCA TGGTGATGCG GTTTTGGCAG TACATCAATG GGCGTGGATA	420
GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCCAT TACGTCAATG GGAGTTTGTT	480
TTGGCACCAA AATCAACGGG ACTTTCCAAA ATGTCGTAAC AACTCCGCCC CATTGACGCA	540
AATGGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC AGAGCTCTCT GGCTAACTAG	600
AGAACCCACT GCTTAACTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG	660
CTTCTGCAGG TCGACATCGA TGGATCCGGT ACCTCGAGCG CGAATTCTCT AGAGGATCTT	720
TGTGAAGGAA CTTACTTCT GTGGTGTGAC ATAATTGGAC AACTACCTA CAGAGATTTA	780
AAGCTCTAAG GTAAATATAA AATTTTTAAG TGTATAATGT GTTAACTAC TGATTCTAAT	840
TGTTTGTGTA TTTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC	900
CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG ATGAGGCTAC	960
TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA AAGGTAGAAG ACCCCAAGGA	1020
CTTCCTTCA GAATTGCTAA GTTTTTTGAG TCATGCTGTG TTTAGTAATA GAACTCTTGC	1080
TTGCTTTGCT ATTTACACCA CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA	1140
AAAAATTTTG ATGTATAGTG CCTTGACTAG AGATCATAAT CAGCCATACC ACATTGTAG	1200
AGGTTTTACT TGCTTTAAAA AACCTCCAC ACCTCCCCCT GAACCTGAAA CATAAAATGA	1260
ATGCAATTGT TGTTGTTAAC TTGTTTATTG CAGCTTATAA TGGTTACAAA TAAAGCAATA	1320
GCATCACAAA TTTCACAAAT AAAGCATTTT TTCACTGCA TTCTAGTTGT GGTTTGTCCA	1380
AACTCATCAA TGTATCTTAT CATGTCTGGA TCAATTCTGA GAACTAGCC TTAAAGACAG	1440

FIG. 6B

ACAGCTTTGT TCTAGTCAGC CAGGCAAGCA TATGTAAATA AAGTTCCTCA GGGAACTGAG	1500
GTTAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATT CACGTAACAG AAGATTCCGC	1560
CTCAAGTTCC GGTTAACAAC AGGAGGCAAC GAGATCTCAA ATCTATTACT TCTAATCGGG	1620
TAATTA AAC CTTTCAACTA AAACACGGAC CCACGGATGT CACCCACTTT TCCTTCCCCG	1680
GCTCCGCCCT TCTCAGTACT CCCACCATT AGGCTCGCTA CTCCACCTCC ACTTCCGGGC	1740
GCGACACCCA CGTGCCCTCT CCCACCCGAC GCTAACCCCG CCCCTGCCCG TCTGACCCCG	1800
CCCACCACCT GGCCCCGCCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC GCAGCCAAGG	1860
CGGACGGGTA GACGCTGGGG GCGCTGAGGA GTCGTCCTCT ACCTTCTCTG CTGGCTCGGT	1920
GGGGGACGCG GTGGATCTCA GGCTTCCGGA AGACTGGAAG AACCGGCTCA GAACCGCTTG	1980
TCTCCGCGGG GCTTGGGCGG CGGAAGAATG GCCGCTAGAC GCGGACTTGG TCGGAGGCAT	2040
CGCAGGATGC AGAAGAGCAA GCCCGCCGGG AGCGCGCGGC TGTACTACCC CGCGCCTGGA	2100
GCGGCCACGC CGGACTGGGC GGGGCCGGCC TGGTGGAGGC GGAGTCTGAC CTCGTGGAGG	2160
CGGGGCCTCT GATGTTCAA TAGGATGCTA GGCTTGTTGA GGCCTGGCCT CCGATTACAC	2220
AGTGGGAAGC AGCGCCGGGC GACTGCAATT TCGCGCCAAA CTTGGGGGAA GCACAGCGTA	2280
CAGGCTGCCT AGGTGATCGC TGCTGCTGTC ATGGTTTCGAC CGCTGAACTG CATCGTCGCC	2340
GTGTCCCAGA ATATGGGCAT CGGCAAGAAC GGAGACCTTC CCTGGCCAAT GCTCAGGTAC	2400
TGGCTGGATT GGGTTAGGGA AACCGAGGCG GTTCGCTGAA TCGGGTCGAG CACTTGGCGG	2460
AGACGCGCGG GCCAACTACT TAGGGACAGT CATGAGGGGT AGGCCCCCGG GCTGCTGCCC	2520
TTGCCCATGC CCGCGGTGAT CCCCATGCTG TGCCAGCCTT TGCCCAGAGG CGCTCTAGCT	2580
GGGAGCAAAG TCCGGTCACT GGGCAGCACC ACCCCCCGGA CTTGCATGGG TAGCCGCTGA	2640
GATGGAGCCT GAGCACACGT GACAGGGTCC CTGTTAACGC AGTGTTTCTC TAACTTTCAG	2700
GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGGAAG GTAAACAGAA	2760
CCTGGTGATT ATGGGCCGGA AAACCTGGTT CTCCATTCTT GAGAAGAATC GACCTTTAAA	2820
GGACAGAATT AATATAGTTC TCAGTAGAGA GCTCAAGGAA CCACCACAAG GAGCTCATTT	2880
TCTTGCCAAA AGTCTGGACC ATGCCTTAAA ACTTATTGAA CAACCAGAGT TAGCAGATAA	2940
AGTGGACATG GTTTGGATAG TTGGAGGCAG TTCCGTTTAC AAGGAAGCCA TGAATCAGCC	3000

FIG. 6C

AGGCCATCTC AGACTCTTTG TGACAAGGAT CATGCAGGAA TTTGAAAGTG ACACGTTCTT 3060
 CCCAGAAATT GATTTGGAGA AATATAAACT TCTCCCAGAG TACCCAGGGG TCCTTTCTGA 3120
 AGTCCAGGAG GAAAAAGGCA TCAAGTATAA ATTTGAAGTC TATGAGAAGA AAGGCTAACA 3180
 GAAAGATACT TGCTGATTGA CTTCAAGTTC TACTGCTTTC CTCCTAAAAT TATGCATTTT 3240
 TACAAGACCA TGGGACTTGT GTTGGCTTTA GATCCTGTGC ATCCTGGGCA ACTGTTGTAC 3300
 TCTAAGCCAC TCCCCAAAGT CATGCCCCAG CCCCTGTATA ATTCTAAACA ATTAGAATTA 3360
 TTTTCATTTT CATTAGTCTA ACCAGGTTAT ATTAAATATA CTTTAAGAAA CACCATTGTC 3420
 CATAAGTTC TCAATGCCCC TCCCATGCAG CCTCAAGTGG CTCCCCAGCA GATGCATAGG 3480
 GTAGTGTGTG TACAAGAGAC CCCAAAGACA TAGAGCCCCT GAGAGCATGA GCTGATATGG 3540
 GGGCTCATAG AGATAGGAGC TAGATGAATA AGTACAAAGG GCAGAAATGG GTTTTAACCA 3600
 GCAGAGCTAG AACTCAGACT TTAAAGAAAA TTAGATCAAA GTAGAGACTG AATTATTCTG 3660
 CACATCAGAC TCTGAGCAGA GTTCTGTTCA CTCAGACAGA AAATGGGTAA ATTGAGAGCT 3720
 GGCTCCATTG TGCTCCTTAG AGATGGGAGC AGGTGGAGGA TTATATAAGG TCTGGAACAT 3780
 TTAAGTTCTC CGTTTCTCAT CTTCAAGTGG ATTCCAAGGG ATACTACAAT TCTGTGGAAT 3840
 GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG TATGCAAAGC 3900
 ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA 3960
 AGTATGCAAA GCATGCATCT CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC 4020
 ATCCCGCCCC TAACTCCGCC CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT 4080
 TTTATTTATG CAGAGGCCGA GGCGCCTCTG AGCTATTCCA GAAGTAGTGA GGAGGCTTTT 4140
 TTGGAGGCCT AGGCTTTTGC AAAAAAGCTA ATTCAGCCTG AATGGCGAAT GGGACGCGCC 4200
 CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT 4260
 TGCCAGCGCC CTAGCGCCCG CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG CCACGTTTCG 4320
 CGGCTTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTTA GGGTTCCGAT TTAGTGCTTT 4380
 ACGGCACCTC GACCCCAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC 4440
 TGATAGACGG TTTTTCGCCC TTTGACGTTG GAGTCCACGT TCTTTAATAG TGGACTCTTG 4500
 TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT CTTTGTATTT ATAAGGGATT 4560

FIG. 6D

TTGCCGATTT CGGCCTATTG GTTAAAAAAT GAGCTGATTT AACAAAAATT TAACGCGAAT	4620
TTTAACAAAA TATTAACGTT TACAATTTC A GGTGGCACTT TTCGGGGAAA TGTGCGCGGA	4680
ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA	4740
CCCTGATAAA TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT	4800
GTCGCCCTTA TTCCCTTTTT TCGGCATTT TGCCTTCCTG TTTTGTCTCA CCCAGAAACG	4860
CTGGTGAAAG TAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG	4920
GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTGCCCCG AAGAACGTTT TCCAATGATG	4980
AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG	5040
CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA	5100
GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG	5160
AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC	5220
GCTTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG	5280
AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAACG	5340
TTGCGCAAAC TATTAAGTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC	5400
TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG	5460
TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG	5520
GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT	5580
ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA	5640
CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACTTCA TTTTAAATTT	5700
AAAAGGATCT AGGTGAAGAT CCTTTTTGAT AATCTCATGA CCAAATCCC TTAACGTGAG	5760
TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT	5820
TTTTTCTGCG GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT	5880
TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG	5940
CAGATACCAA AACTGTCTCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT	6000
GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC	6060
GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GCGCAGCGG	6120

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

Year	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

FIG. 7A

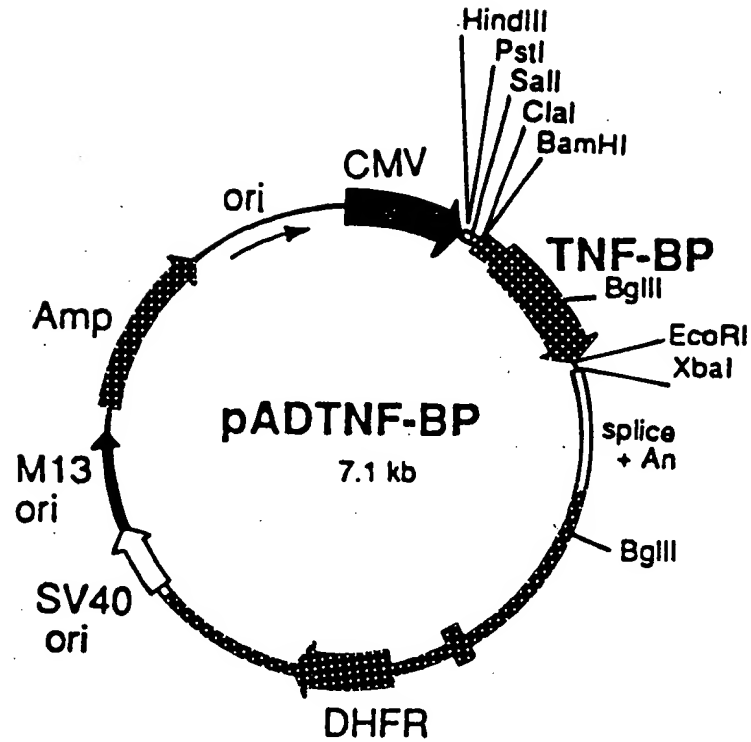


FIG. 7B

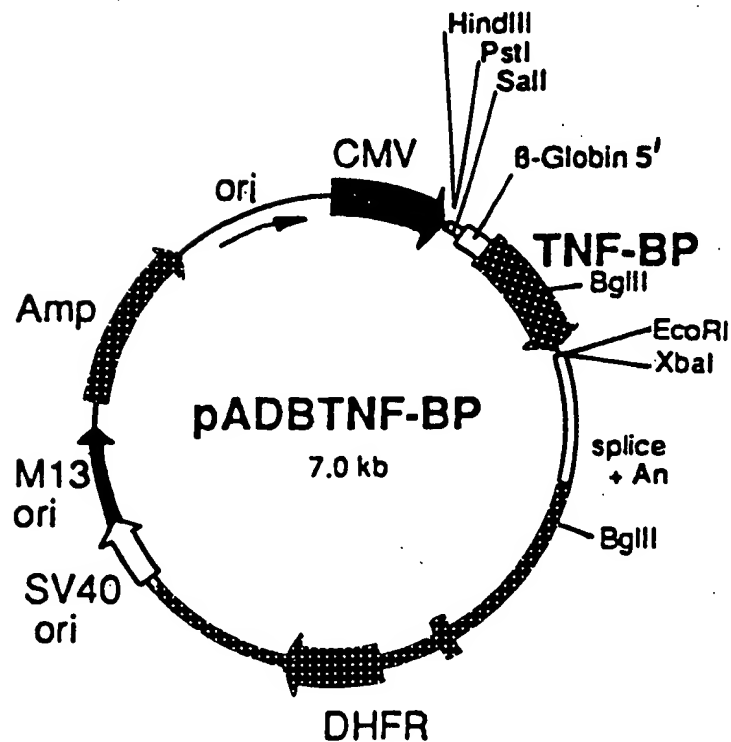


FIG. 7C

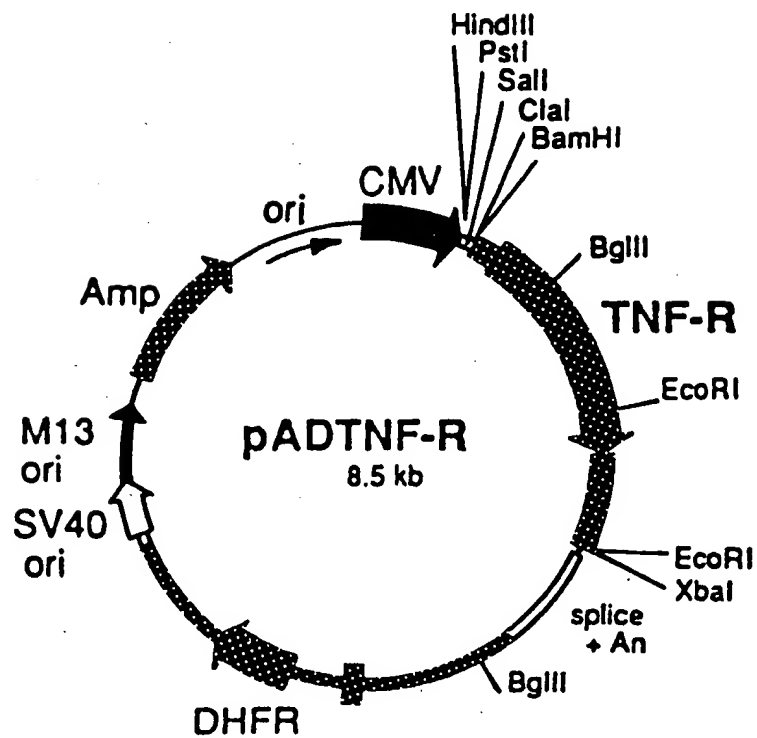


FIG. 7D

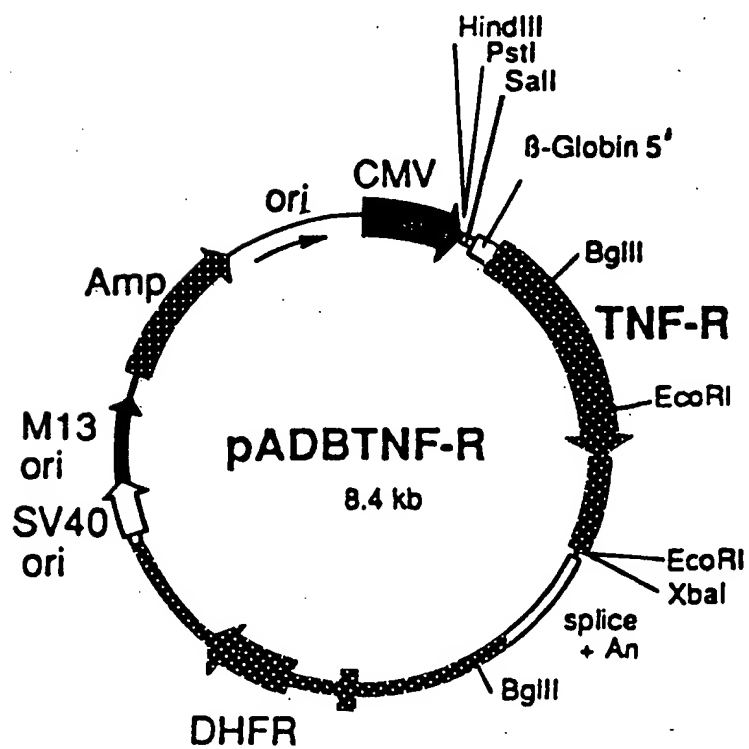


FIG. 8A

raTNF-R

GAATTCCTTT	TCTCCGAGTT	TTCTGAACTC	TGGCTCATGA	TCGGGCTTAC	TGGATACGAG	60
AATCCTGGAG	GACCGTACCC	TGATTTCCAT	CTACCTCTGA	CTTTGAGCCT	TTCTAACCCG	120
GGGCTCACGC	TGCCAACACC	CGGGCCACCT	GGTCCGATCG	TCTTACTTCA	TTCACCAGCG	180
TTGCCAATTG	CTGCCCTGTC	CCCAGCCCCA	ATGGGGGAGT	GAGAGAGGCC	ACTGCCGGCC	240
GGAC						
245/1				275/11		
ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC CTG GCT CTG CTG ATG						
Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu Ala Leu Leu Met						
305/21				335/31		
GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG						
Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro Ser Leu Gly Asp Arg Glu Lys Arg						
365/41				395/51		
GAT AAT TTG TGT CCC CAG GGA AAG TAT GGC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC						
Asp Asn Leu Cys Pro Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr						
425/61				455/71		
AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA GGG CAG GAA ACA GTC						
Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val						
485/81				515/91		
TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC						
Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val Arg Gln Cys Leu						
545/101				575/111		
AGT TGC AAG ACA TGT CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC						
Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp						
605/121				635/131		
ATG GAC ACC GTG TGT GGC TGC AAG AAG AAC CAA TTC CAG CGC TAC CTG AGT GAG ACG CAT						
Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His						
665/141				695/151		
TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG						
Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu						
725/161				755/171		
AAA CAG AAC ACC GTG TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC						
Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr						
785/181				815/191		
CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC CTA CCT CCA GTT GCA						
Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys Leu Pro Pro Val Ala						
845/201				875/211		
AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT GCC GTG CTG TTG CCT CTG GTT ATC TTC CTA						
Asn Val Thr Asn Pro Gln Asp Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu						
905/221				935/231		
GGT CTT TGC CTT TTA TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG						
Gly Leu Cys Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg						
965/241				995/251		
CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA GAG GTG GAG GGT GAA						
Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu Val Glu Gly Glu						
1025/261				1055/271		
GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC						
Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly						
1085/281				1115/291		
TTC AAC CCC ACT CTG GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC						
Phe Asn Pro Thr Leu Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr						
1145/301				1175/311		
CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG CCA CCT GTA AGA GAG						
Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu						
1205/321				1235/331		
GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC						
Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile						

FIG. 8A

FIG. 8B

1265/341 1295/351
CCC GCC CCT GTT CGG AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT
Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
1325/361 1355/371
GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG ACA CGC TGG AAG GAG
Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu
1385/381 1415/391
TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC GAG ATC GAG CGG CTG GAG CTG CAG AAC GGG
Phe Met Arg Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly
1445/401 1475/411
CGT TGC CTC CGC GAG GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA
Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
1505/421 1535/431
CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG AAC CTG CGT GGC TGC
His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met Asn Leu Arg Gly Cys
1565/441 1595/451
CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG
Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro
1625/461
CGA TAA
Arg Stop
GGCCACACCC CCACCTCAGG AACGGGACTC GAAGGACCAT CCTGCTAGAT 1680
GCCCTGCTTC CCTGTGAACC TCCTCTTTGG TCCTCTAGGG GGCAGGCTCG ATCTGGCAGG 1740
CTCGATCTGG CAGCCACTTC CTTGGTGCTA CCGACTTGGT GTACATAGCT TTTCCCAGCT 1800
GCCGAGGACA GCCTGTGCCA GCCACTTGTG CATGGCAGGG AAGTGTGCCA TCTGCTCCCA 1860
GACAGCTGAG GGTGCCAAAA GCCAGGAGAG GTGATTGTGG AGAAAAAGCA CAATCTATCT 1920
GATACCCACT TGGGATGCAA GGACCCAAAC AAAGCTTCTC AGGGCCTCCT CAGTTGATTT 1980
CTGGGGCCCTT TTCACAGTAG ATAAACAGT CTTTGTATTG ATTATATCAC ACTAATGGAT 2040
GAACGGTTGA ACTCCCTAAG GTAGGGGCAA GCACAGAACA GTGGGGTCTC CAGCTGGAGC 2100
CCCCGACTCT TGTAATACA CTAAAAATCT AAAAGTGAAA AAAAAAAAAA AAAAAAAAAA 2160
AAAAAAGGAA TTC

1265/341 1295/351

FIG. 9B

1233/341 1263/351
TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC
Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
1293/361 1323/371
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG
Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu
1353/381 1383/391
AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA
Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
1413/401 1443/411
TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu
1473/421 1503/431
CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG
Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala
1533/441 1563/451
CTT TGC GGC CCC GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGA 1580
Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg Stop

GGCTGCGCCC CTGCGGGCAG CTCTAAGGAC CGTCCTGCGA 1620
GATCGCCTTC CAACCCCACT TTTTCTGGA AAGGAGGGGT CCTGCAGGGG CAAGCAGGAG 1680
CTAGCAGCCG CCTACTTGGT GCTAACCCT CGATGTACAT AGCTTTTCTC AGCTGCCTGC 1740
GCGCCGCCGA CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT 1800
GAGTGGGTGG TTTGCGAGGA TGAGGGACGC TATGCCTCAT GCCCGTTTTG GGTGTCCTCA 1860
CCAGCAAGGC TGCTCGGGGG CCCCTGGTTC GTCCCTGAGC CTTTTTCACA GTGCATAAGC 1920
AGTTTTTTTT GTTTTGTGT TGTGTTGTTT TGTTTTTAAA TCAATCATGT TACACTAATA 1980
GAACTTGGC ACTCCTGTGC CCTCTGCCTG GACAAGCACA TAGCAAGCTG AACTGTCCTA 2040
AGGCAGGGGC GAGCACGGAA CAATGGGGCC TTCAGCTGGA GCTGTGGACT TTTGTACATA 2100
CACTAAAATT CTGAAGTTAA AAAAAAAAAA AAAAGGAATT C 2141

1233/341 1263/351 1323/371 1383/391 1443/411 1503/431 1563/451

FIG.10

